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Stochastic Modeling of Regulation of Gene Expression by Multiple Competing Small RNAs CHARLES BAKER, TAO JIA, RAHUL KULKARNI, Virginia Polytechnic Institute and State University — A wealth of new research has highlighted the critical roles of small RNAs (sRNAs) in diverse processes such as quorum sensing and cellular responses to stress. The pathways controlling these processes often have a central motif comprised of a key protein regulated by multiple sRNAs. However, the regulation of stochastic gene expression of a single target gene by multiple sRNAs is currently not well understood. To address this issue, we analyze a stochastic model of regulation of gene expression by multiple sRNAs. For this model, we derive exact analytic results for the regulated protein distribution including compact expressions for its mean and variance. The derived results provide novel insights into the roles of multiple sRNAs in fine-tuning the noise in gene expression. In particular, we show that, in contrast to regulation by a single sRNA, multiple sRNAs provide a mechanism for independently controlling the mean and variance of the regulated protein distribution.

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